SEQUENCE LISTING

<110> Allain, Eric
Wenger, Kevin S
Bisgård-Frantzen, Henrik

<120> Process for producing a fermentation product

<130> 10674.000-US

<160> 41

<170> PatentIn version 3.3

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atg ttt cgt tca ctc ctg gcc ttg gct gcg tgt gca gtc gcc tct gta       48
Met Phe Arg Ser Leu Leu Ala Leu Ala Ala Cys Ala Val Ala Ser Val
            -15                 -10                 -5

tct gca cag tct gcg tct gcg aca gca tat ctt acc aag gaa tct gca       96
Ser Ala Gln Ser Ala Ser Ala Thr Ala Tyr Leu Thr Lys Glu Ser Ala
    -1  1               5                   10

gtt gcc aag aat ggc gta ctt tgc aac att ggt agc cag gga tgc atg      144
Val Ala Lys Asn Gly Val Leu Cys Asn Ile Gly Ser Gln Gly Cys Met
15                  20                  25                  30

tct gag ggt gcc tat agc ggt att gtg atc gca tct ccc tct aaa act      192
Ser Glu Gly Ala Tyr Ser Gly Ile Val Ile Ala Ser Pro Ser Lys Thr
                35                  40                  45

agc cct gac tat ctc t gtgagtatta tttgtaaagt agcctcactg atagtacatt    248
Ser Pro Asp Tyr Leu
            50

ttctgagttc tgttacaacc ctggtattat aatag at  acc tgg act cgc gac       300
                                    Tyr Thr Trp Thr Arg Asp
                                                55

tcg tcg ctc gtc ttc aag atg tta att gac caa tac aca aat ggc ctg      348
Ser Ser Leu Val Phe Lys Met Leu Ile Asp Gln Tyr Thr Asn Gly Leu
        60                  65                  70

gat acg gtatgtggca tcngcgttcc ggctcgcctc aaagatgnaa aattgatgtt      404
Asp Thr
    75

tcttag aca ctg cgc act ctc att gac gag ttt gtc tct gcg gaa gcc       452
       Thr Leu Arg Thr Leu Ile Asp Glu Phe Val Ser Ala Glu Ala
                    80                  85

acc att caa caa acc agt aac cca tct ggt acc gtc tct acc ggt ggt      500
Thr Ile Gln Gln Thr Ser Asn Pro Ser Gly Thr Val Ser Thr Gly Gly
90                  95                  100                 105

ctc ggc gaa ccc aaa ttc aat atc gac gag acg gca ttt acg ggc gca      548
Leu Gly Glu Pro Lys Phe Asn Ile Asp Glu Thr Ala Phe Thr Gly Ala
                110                 115                 120

tgg ggt cgt gtaagctacc aatacacaat caaaatcgac catctgtatt              597
Trp Gly Arg

tactatctat aatttctag ccc caa cgt gat ggt ccc gcc ctc cgt gca acc      649
                    Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr
                    125                 130                 135

gca atc atg acc tat gcg acg tat ctg tac aac aat ggc aac act tcc      697
Ala Ile Met Thr Tyr Ala Thr Tyr Leu Tyr Asn Asn Gly Asn Thr Ser
                140                 145                 150
```

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tac gtg acc aac acc ctt tgg cct atc atc aag ctc gac ctt gac tat      745
Tyr Val Thr Asn Thr Leu Trp Pro Ile Ile Lys Leu Asp Leu Asp Tyr
            155                 160                 165

gtc aac tcg gac tgg aac cag acc a gtaagcgaat ttctaggggg              790
Val Asn Ser Asp Trp Asn Gln Thr
        170                 175

acttatctaa aacagcatat tcaaccagta aatag cg  ttt gac ctc tgg gaa       842
                                       Thr Phe Asp Leu Trp Glu
                                                       180

gaa gtt gac tcg tct tct ttc ttt acg act gcc gtt cag cac cgt gct      890
Glu Val Asp Ser Ser Ser Phe Phe Thr Thr Ala Val Gln His Arg Ala
            185                 190                 195

ctt gtt cag ggc gca gcc ttt gct acc ctc atc ggc caa act tcg tct      938
Leu Val Gln Gly Ala Ala Phe Ala Thr Leu Ile Gly Gln Thr Ser Ser
        200                 205                 210

gct tcg act tac tcc gcc acg gcc cct agc att ctc tgc ttc ttg cag      986
Ala Ser Thr Tyr Ser Ala Thr Ala Pro Ser Ile Leu Cys Phe Leu Gln
    215                 220                 225

gtgagataaa aatctttcta tgtaattggt ttttcccctc aaattgaaat tgacatattt   1046

gcgatccaat ag tct tac tgg aac acc aac gga tac tgg acg gcc aac act    1097
             Ser Tyr Trp Asn Thr Asn Gly Tyr Trp Thr Ala Asn Thr
             230                 235                 240

ggt ggc gga cgt tcc ggc aag gac gcc aac acc ata ctc gct tct atc     1145
Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Ile Leu Ala Ser Ile
        245                 250                 255

cac aca ttt gac gcc agc gcc ggc tgc tct gct gcc acg tct caa cca     1193
His Thr Phe Asp Ala Ser Ala Gly Cys Ser Ala Ala Thr Ser Gln Pro
    260                 265                 270

tgc tct gac gta gca ttg gcc aac ctg aag gta tac gtt gac tct ttc     1241
Cys Ser Asp Val Ala Leu Ala Asn Leu Lys Val Tyr Val Asp Ser Phe
275                 280                 285                 290

cgt agt att tat acg atc aac agc ggt att tcc tct acc tcg ggt gtt     1289
Arg Ser Ile Tyr Thr Ile Asn Ser Gly Ile Ser Ser Thr Ser Gly Val
                295                 300                 305

gct act ggt cgc tac ccc gaa gat tcg tat tac aat ggc aac             1331
Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Tyr Asn Gly Asn
            310                 315                 320

gtacgtattt atctaatttt tccaagacag tcaaagttta tgttcatctg ccccctttta   1391

cctgtacatt caaaatag ccc tgg tac ctc tgc aca ctc gcc gtc gcc gag      1442
                   Pro Trp Tyr Leu Cys Thr Leu Ala Val Ala Glu
                                   325                 330

cag ctc tat gat gct ctc atc gta tgg aag gct gcc ggg gag ctc aac     1490
```

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Gln Leu Tyr Asp Ala Leu Ile Val Trp Lys Ala Ala Gly Glu Leu Asn
            335                 340                 345

gtc acc tcc gtc tcg ctc gcg ttc ttc cag caa ttc gac tcg agc atc     1538
Val Thr Ser Val Ser Leu Ala Phe Phe Gln Gln Phe Asp Ser Ser Ile
        350                 355                 360

acc gcc ggc act tac gcc tcc tcg tcg agc gta tac act tcg ctc atc     1586
Thr Ala Gly Thr Tyr Ala Ser Ser Ser Ser Val Tyr Thr Ser Leu Ile
    365                 370                 375

tct gac atc cag gcg ttc gca gac gag ttt gtt gac att gtt gcc aag     1634
Ser Asp Ile Gln Ala Phe Ala Asp Glu Phe Val Asp Ile Val Ala Lys
380                 385                 390                 395

tac acg cct tcg tct ggc ttc ttg tct gag cag tat gat aag tcc acg     1682
Tyr Thr Pro Ser Ser Gly Phe Leu Ser Glu Gln Tyr Asp Lys Ser Thr
                400                 405                 410

ggt gct cag gat tcg gct gct aac ttg act t gtaagtcatc tatttgttca     1733
Gly Ala Gln Asp Ser Ala Ala Asn Leu Thr
            415                 420

ttctattcct tttcaaaaaa aaaagtgatg ctaatgattt ttggcggaaa ccag gg      1789
                                                              Trp


tcc tat gct gct gct atc acc gct tac caa gcc cgc aat ggc ttc aca     1837
Ser Tyr Ala Ala Ala Ile Thr Ala Tyr Gln Ala Arg Asn Gly Phe Thr
        425                 430                 435

ggt gct tcg tgg ggt gct aag gga gtt tct acc tcc tgc tcg act ggt     1885
Gly Ala Ser Trp Gly Ala Lys Gly Val Ser Thr Ser Cys Ser Thr Gly
    440                 445                 450

gct aca agc ccg ggt ggc tcc tcg ggt agt gtc gag gtc act ttc gac     1933
Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp
455                 460                 465                 470

gtt tac gct acc aca gta tat ggc c gtaagcactt gactagcttc              1978
Val Tyr Ala Thr Thr Val Tyr Gly
                475

aaaccatact tcatcatgct gataaacaaa aaaatgaaac ag ag  aac atc tat      2031
                                              Gln Asn Ile Tyr
                                                  480

atc acc ggt gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat ggt     2079
Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly
        485                 490                 495

gtt gca ctc tct tct gct aac tac ccc acc tgg agt g gtaagttgac       2126
Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser
    500                 505                 510

ccttaccagt atcttgacag acattgatat tgacttccgc aatacag cc  acg atc    2181
                                                  Ala Thr Ile
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gct ctc ccc gct gac acg aca atc cag tac aag tat gtc aac att gac     2229
Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp
    515                 520                 525

ggc agc acc gtc atc tgg gag gat gct atc agc aat cgc gag atc acg     2277
Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr
530                 535                 540                 545

acg ccc gcc agc ggc aca tac acc gaa aaa gac act tgg gat gaa tct     2325
Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
                550                 555                 560

taaactgctg aacttgaacg gcttgcaaaa gcgaatggtg tagaaaataa acgaagattt   2385

tgattgcttt gttttgtttc tcttcctatc ttgtttctct ag                     2427
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<210> 2
<211> 579
<212> PRT
<213> Athelia rolfsii

<400> 2

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Met Phe Arg Ser Leu Leu Ala Leu Ala Ala Cys Ala Val Ala Ser Val
            -15                 -10                 -5

Ser Ala Gln Ser Ala Ser Ala Thr Ala Tyr Leu Thr Lys Glu Ser Ala
    -1  1               5                   10

Val Ala Lys Asn Gly Val Leu Cys Asn Ile Gly Ser Gln Gly Cys Met
15                  20                  25                  30

Ser Glu Gly Ala Tyr Ser Gly Ile Val Ile Ala Ser Pro Ser Lys Thr
                35                  40                  45

Ser Pro Asp Tyr Leu Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe
            50                  55                  60

Lys Met Leu Ile Asp Gln Tyr Thr Asn Gly Leu Asp Thr Thr Leu Arg
        65                  70                  75

Thr Leu Ile Asp Glu Phe Val Ser Ala Glu Ala Thr Ile Gln Gln Thr
    80                  85                  90

Ser Asn Pro Ser Gly Thr Val Ser Thr Gly Gly Leu Gly Glu Pro Lys
95                  100                 105                 110
```

```
Phe Asn Ile Asp Glu Thr Ala Phe Thr Gly Ala Trp Gly Arg Pro Gln
                115                 120                 125

Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Ile Met Thr Tyr Ala Thr
            130                 135                 140

Tyr Leu Tyr Asn Asn Gly Asn Thr Ser Tyr Val Thr Asn Thr Leu Trp
        145                 150                 155

Pro Ile Ile Lys Leu Asp Leu Asp Tyr Val Asn Ser Asp Trp Asn Gln
    160                 165                 170

Thr Thr Phe Asp Leu Trp Glu Glu Val Asp Ser Ser Ser Phe Phe Thr
175                 180                 185                 190

Thr Ala Val Gln His Arg Ala Leu Val Gln Gly Ala Ala Phe Ala Thr
                195                 200                 205

Leu Ile Gly Gln Thr Ser Ser Ala Ser Thr Tyr Ser Ala Thr Ala Pro
            210                 215                 220

Ser Ile Leu Cys Phe Leu Gln Ser Tyr Trp Asn Thr Asn Gly Tyr Trp
        225                 230                 235

Thr Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Ile
    240                 245                 250

Leu Ala Ser Ile His Thr Phe Asp Ala Ser Ala Gly Cys Ser Ala Ala
255                 260                 265                 270

Thr Ser Gln Pro Cys Ser Asp Val Ala Leu Ala Asn Leu Lys Val Tyr
                275                 280                 285

Val Asp Ser Phe Arg Ser Ile Tyr Thr Ile Asn Ser Gly Ile Ser Ser
            290                 295                 300

Thr Ser Gly Val Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Tyr Asn
        305                 310                 315

Gly Asn Pro Trp Tyr Leu Cys Thr Leu Ala Val Ala Glu Gln Leu Tyr
    320                 325                 330
```

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Asp Ala Leu Ile Val Trp Lys Ala Ala Gly Glu Leu Asn Val Thr Ser
335                 340                 345                 350

Val Ser Leu Ala Phe Phe Gln Gln Phe Asp Ser Ser Ile Thr Ala Gly
                355                 360                 365

Thr Tyr Ala Ser Ser Ser Ser Val Tyr Thr Ser Leu Ile Ser Asp Ile
            370                 375                 380

Gln Ala Phe Ala Asp Glu Phe Val Asp Ile Val Ala Lys Tyr Thr Pro
        385                 390                 395

Ser Ser Gly Phe Leu Ser Glu Gln Tyr Asp Lys Ser Thr Gly Ala Gln
    400                 405                 410

Asp Ser Ala Ala Asn Leu Thr Trp Ser Tyr Ala Ala Ala Ile Thr Ala
415                 420                 425                 430

Tyr Gln Ala Arg Asn Gly Phe Thr Gly Ala Ser Trp Gly Ala Lys Gly
                435                 440                 445

Val Ser Thr Ser Cys Ser Thr Gly Ala Thr Ser Pro Gly Gly Ser Ser
            450                 455                 460

Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly
        465                 470                 475

Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr
    480                 485                 490

Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser
495                 500                 505                 510

Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val
                515                 520                 525

Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg
            530                 535                 540

Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp
        545                 550                 555

Asp Glu Ser
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560

<210> 3
<211> 484
<212> PRT
<213> Aspergillus niger

<220>
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<222> (1)..(484)

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1 5 10 15

Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asn Thr
20 25 30

Gly Asn Glu Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asp His
35 40 45

Leu Asp Tyr Ile Glu Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
50 55 60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65 70 75 80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
85 90 95

Ala Asp Asn Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
100 105 110

Tyr Leu Met Val Asp Val Val Pro Asp His Met Gly Tyr Ala Gly Asn
115 120 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
130 135 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145 150 155 160

Val Glu Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
165 170 175

```
Asp Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205

Leu Glu Val Gln Pro Asp Phe Phe Pro Gly Tyr Asn Lys Ala Ser Gly
    210                 215                 220

Val Tyr Cys Val Gly Glu Ile Asp Asn Gly Asn Pro Ala Ser Asp Cys
225                 230                 235                 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Lys Tyr
    290                 295                 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ala
                325                 330                 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365

Arg Lys Leu Ala Ile Ala Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
    370                 375                 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Ala Lys Gly Thr
385                 390                 395                 400
```

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465 470 475 480

Leu Tyr Val Glu

<210> 4
<211> 498
<212> PRT
<213> Aspergillus oryzae

<220>
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<222> (1)..(19)

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<222> (20)..(498)

<400> 4

Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala
-15 -10 -5

Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
-1 1 5 10

Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
15 20 25

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
30 35 40 45

```
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
                50                  55                  60

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
            65                  70                  75

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
        80                  85                  90

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
    95                  100                 105

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
110                 115                 120                 125

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
                130                 135                 140

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
            145                 150                 155

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
        160                 165                 170

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
    175                 180                 185

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
190                 195                 200                 205

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
                210                 215                 220

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
            225                 230                 235

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
        240                 245                 250

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
    255                 260                 265

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
```

270 275 280 285

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
290 295 300

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
305 310 315

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
320 325 330

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
335 340 345

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
350 355 360 365

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
370 375 380

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
385 390 395

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
400 405 410

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
415 420 425

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
430 435 440 445

Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
450 455 460

Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
465 470 475

Ser Ser

<210> 5
<211> 483

<212> PRT
<213> Bacillus licheniformis

<220>
<221> mat_peptide
<222> (1)..(483)

<400> 5

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Arg

<210> 6
<211> 480
<212> PRT
<213> Bacillus amyloliquefaciens

<220>
<221> mat_peptide
<222> (1)..(480)

<400> 6

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
1 5 10 15

Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60

Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp

100 105 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
115 120 125

Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
130 135 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145 150 155 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
165 170 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
195 200 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210 215 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
275 280 285

His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305 310 315 320

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

```
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                 345                 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                 360                 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
    370                 375                 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385                 390                 395                 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
        435                 440                 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
    450                 455                 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465                 470                 475                 480
```

<210> 7
<211> 514
<212> PRT
<213> Bacillus stearothermophilus

<220>
<221> mat_peptide
<222> (1)..(514)

<400> 7

```
Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
1               5                   10                  15

Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
            20                  25                  30
```

```
Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
        35                  40                  45

Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
    50                  55                  60

Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr
65                  70                  75                  80

Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
                85                  90                  95

Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
            100                 105                 110

Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
        115                 120                 125

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
    130                 135                 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
145                 150                 155                 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
                165                 170                 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
            180                 185                 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
        195                 200                 205

Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn
    210                 215                 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
225                 230                 235                 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly
                245                 250                 255
```

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
260 265 270

Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp
275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr
290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val
405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr

485 490 495

Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
500 505 510

Ala Trp

<210> 8
<211> 38
<212> PRT
<213> Aspergillus niger

<220>
<221> MISC_FEATURE
<222> (1)..(38)
<223> linker sequence

<400> 8

Thr Gly Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val
1 5 10 15

Thr Ser Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser
20 25 30

Thr Ser Ser Thr Ser Ala
35

<210> 9
<211> 31
<212> PRT
<213> Aspergillus kawachi

<220>
<221> MISC_FEATURE
<222> (1)..(31)
<223> linker sequence

<400> 9

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
1 5 10 15

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser
20 25 30

<210> 10
<211> 11
<212> PRT
<213> Athelia rolfsii

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> linker sequence

<400> 10

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser
1 5 10

<210> 11
<211> 8
<212> PRT
<213> Artificial

<220>
<223> PEPT linker

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> linker sequence

<400> 11

Pro Glu Pro Thr Pro Glu Pro Thr
1 5

<210> 12
<211> 396
<212> DNA
<213> Aspergillus kawachi

<220>
<221> CDS
<222> (1)..(396)
<223> CBM

<400> 12
act agt aca tcc aaa gcc acc acc tcc tct tct tct tct tct gct gct 48
Thr Ser Thr Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala
1 5 10 15

gct act act tct tca tca tgc acc gca aca agc acc acc ctc ccc atc 96
Ala Thr Thr Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile
20 25 30

```
acc ttc gaa gaa ctc gtc acc act acc tac ggg gaa gaa gtc tac ctc      144
Thr Phe Glu Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu
        35                  40                  45

agc gga tct atc tcc cag ctc gga gag tgg gat acg agt gac gcg gtg      192
Ser Gly Ser Ile Ser Gln Leu Gly Glu Trp Asp Thr Ser Asp Ala Val
    50                  55                  60

aag ttg tcc gcg gat gat tat acc tcg agt aac ccc gag tgg tct gtt      240
Lys Leu Ser Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val
65                  70                  75                  80

act gtg tcg ttg ccg gtg ggg acg acc ttc gag tat aag ttt att aag      288
Thr Val Ser Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys
                85                  90                  95

gtc gat gag ggt gga agt gtg act tgg gaa agt gat ccg aat agg gag      336
Val Asp Glu Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu
            100                 105                 110

tat act gtg cct gaa tgt ggg aat ggg agt ggg gag acg gtg gtt gat      384
Tyr Thr Val Pro Glu Cys Gly Asn Gly Ser Gly Glu Thr Val Val Asp
        115                 120                 125

acg tgg agg tag                                                     396
Thr Trp Arg
    130
```

<210> 13
<211> 131
<212> PRT
<213> Aspergillus kawachi

<400> 13

```
Thr Ser Thr Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala
1               5                   10                  15

Ala Thr Thr Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile
            20                  25                  30

Thr Phe Glu Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu
        35                  40                  45

Ser Gly Ser Ile Ser Gln Leu Gly Glu Trp Asp Thr Ser Asp Ala Val
    50                  55                  60

Lys Leu Ser Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val
65                  70                  75                  80

Thr Val Ser Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys
```

85 90 95

Val Asp Glu Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu
100 105 110

Tyr Thr Val Pro Glu Cys Gly Asn Gly Ser Gly Glu Thr Val Val Asp
115 120 125

Thr Trp Arg
130

<210> 14
<211> 102
<212> PRT
<213> Bacillus flavothermus

<220>
<221> MISC_FEATURE
<222> (1)..(102)
<223> CBM

<400> 14

Ile Ser Thr Thr Ser Gln Ile Thr Phe Thr Val Asn Asn Ala Thr Thr
1 5 10 15

Val Trp Gly Gln Asn Val Tyr Val Val Gly Asn Ile Ser Gln Leu Gly
20 25 30

Asn Trp Asp Pro Val His Ala Val Gln Met Thr Pro Ser Ser Tyr Pro
35 40 45

Thr Trp Thr Val Thr Ile Pro Leu Leu Gln Gly Gln Asn Ile Gln Phe
50 55 60

Lys Phe Ile Lys Lys Asp Ser Ala Gly Asn Val Ile Trp Glu Asp Ile
65 70 75 80

Ser Asn Arg Thr Tyr Thr Val Pro Thr Ala Ala Ser Gly Ala Tyr Thr
85 90 95

Ala Ser Trp Asn Val Pro
100

<210> 15

<211> 99
<212> PRT
<213> Bacillus sp.

<220>
<221> MISC_FEATURE
<222> (1)..(99)
<223> CBM

<400> 15

Thr Ser Asn Val Thr Phe Thr Val Asn Asn Ala Thr Thr Val Tyr Gly
1 5 10 15

Gln Asn Val Tyr Val Val Gly Asn Ile Pro Glu Leu Gly Asn Trp Asn
20 25 30

Ile Ala Asn Ala Ile Gln Met Thr Pro Ser Ser Tyr Pro Thr Trp Lys
35 40 45

Thr Thr Val Ser Leu Pro Gln Gly Lys Ala Ile Glu Phe Lys Phe Ile
50 55 60

Lys Lys Asp Ser Ala Gly Asn Val Ile Trp Glu Asn Ile Ala Asn Arg
65 70 75 80

Thr Tyr Thr Val Pro Phe Ser Ser Thr Gly Ser Tyr Thr Ala Asn Trp
85 90 95

Asn Val Pro

<210> 16
<211> 102
<212> PRT
<213> Alcaliphilic Bacillus

<220>
<221> MISC_FEATURE
<222> (1)..(102)
<223> CBM

<400> 16

Thr Ser Thr Thr Ser Gln Ile Thr Phe Thr Val Asn Asn Ala Thr Thr
1 5 10 15

```
Val Trp Gly Gln Asn Val Tyr Val Val Gly Asn Ile Ser Gln Leu Gly
            20                  25                  30

Asn Trp Asp Pro Val Asn Ala Val Gln Met Thr Pro Ser Ser Tyr Pro
        35                  40                  45

Thr Trp Val Val Thr Val Pro Leu Pro Gln Ser Gln Asn Ile Gln Phe
    50                  55                  60

Lys Phe Ile Lys Lys Asp Gly Ser Gly Asn Val Ile Trp Glu Asn Ile
65                  70                  75                  80

Ser Asn Arg Thr Tyr Thr Val Pro Thr Ala Ala Ser Gly Ala Tyr Thr
                85                  90                  95

Ala Asn Trp Asn Val Pro
            100
```

<210> 17
<211> 112
<212> PRT
<213> Hormoconis resinae

<220>
<221> MISC_FEATURE
<222> (1)..(112)
<223> CBM

<400> 17

```
Cys Gln Val Ser Ile Thr Phe Asn Ile Asn Ala Thr Thr Tyr Tyr Gly
1               5                   10                  15

Glu Asn Leu Tyr Val Ile Gly Asn Ser Ser Asp Leu Gly Ala Trp Asn
            20                  25                  30

Ile Ala Asp Ala Tyr Pro Leu Ser Ala Ser Ala Tyr Thr Gln Asp Arg
        35                  40                  45

Pro Leu Trp Ser Ala Ala Ile Pro Leu Asn Ala Gly Glu Val Ile Ser
    50                  55                  60

Tyr Gln Tyr Val Arg Gln Glu Asp Cys Asp Gln Pro Tyr Ile Tyr Glu
65                  70                  75                  80
```

Thr Val Asn Arg Thr Leu Thr Val Pro Ala Cys Gly Gly Ala Ala Val
85 90 95

Thr Thr Asp Asp Ala Trp Met Gly Pro Val Gly Ser Ser Gly Asn Cys
100 105 110

<210> 18
<211> 95
<212> PRT
<213> Lentinula edodes

<220>
<221> MISC_FEATURE
<222> (1)..(95)
<223> CBM

<400> 18

Val Ser Val Thr Phe Asn Val Asp Ala Ser Thr Leu Glu Gly Gln Asn
1 5 10 15

Val Tyr Leu Thr Gly Ala Val Asp Ala Leu Glu Asp Trp Ser Thr Asp
20 25 30

Asn Ala Ile Leu Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Val Thr
35 40 45

Val Asp Leu Pro Gly Ser Thr Asp Val Gln Tyr Lys Tyr Ile Lys Lys
50 55 60

Asp Gly Ser Gly Thr Val Thr Trp Glu Ser Asp Pro Asn Met Glu Ile
65 70 75 80

Thr Thr Pro Ala Asn Gly Thr Tyr Ala Thr Asn Asp Thr Trp Arg
85 90 95

<210> 19
<211> 107
<212> PRT
<213> Neurospora crassa

<220>
<221> MISC_FEATURE
<222> (1)..(107)
<223> CBM

<400> 19

```
Cys Ala Ala Asp His Glu Val Leu Val Thr Phe Asn Glu Lys Val Thr
1               5                  10                  15

Thr Ser Tyr Gly Gln Thr Val Lys Val Val Gly Ser Ile Ala Ala Leu
            20                  25                  30

Gly Asn Trp Ala Pro Ala Ser Gly Val Thr Leu Ser Ala Lys Gln Tyr
        35                  40                  45

Ser Ser Ser Asn Pro Leu Trp Ser Thr Thr Ile Ala Leu Pro Gln Gly
    50                  55                  60

Thr Ser Phe Lys Tyr Lys Tyr Val Val Val Asn Ser Asp Gly Ser Val
65                  70                  75                  80

Lys Trp Glu Asn Asp Pro Asp Arg Ser Tyr Ala Val Gly Thr Asp Cys
                85                  90                  95

Ala Ser Thr Ala Thr Leu Asp Asp Thr Trp Arg
            100                 105
```

<210> 20
<211> 115
<212> PRT
<213> Talaromyces byssochlamydioides

<220>
<221> MISC_FEATURE
<222> (1)..(115)
<223> CBM

<400> 20

```
Thr Thr Thr Gly Ala Ala Pro Cys Thr Thr Pro Thr Thr Val Ala Val
1               5                  10                  15

Thr Phe Asp Glu Ile Val Thr Thr Thr Tyr Gly Glu Thr Val Tyr Leu
            20                  25                  30

Ser Gly Ser Ile Pro Ala Leu Gly Asn Trp Asp Thr Ser Ser Ala Ile
        35                  40                  45

Ala Leu Ser Ala Val Asp Tyr Thr Ser Ser Asn Pro Leu Trp Tyr Val
    50                  55                  60
```

```
Thr Val Asn Leu Pro Ala Gly Thr Ser Phe Glu Tyr Lys Phe Phe Val
65                  70                  75                  80

Gln Gln Thr Asp Gly Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser
                85                  90                  95

Tyr Thr Val Pro Ala Asn Cys Gly Gln Thr Thr Ala Ile Ile Asp Asp
            100                 105                 110

Ser Trp Gln
        115
```

<210> 21
<211> 115
<212> PRT
<213> Geosmithia cylindrospora

<220>
<221> MISC_FEATURE
<222> (1)..(115)
<223> CBM

<400> 21

```
Thr Ser Thr Gly Ser Ala Pro Cys Thr Thr Pro Thr Thr Val Ala Val
1               5                   10                  15

Thr Phe Asp Glu Ile Val Thr Thr Ser Tyr Gly Glu Thr Val Tyr Leu
            20                  25                  30

Ala Gly Ser Ile Ala Ala Leu Gly Asn Trp Asp Thr Asn Ser Ala Ile
        35                  40                  45

Ala Leu Ser Ala Ala Asp Tyr Thr Ser Asn Asn Asn Leu Trp Tyr Val
    50                  55                  60

Thr Val Asn Leu Ala Ala Gly Thr Ser Phe Gln Tyr Lys Phe Phe Val
65                  70                  75                  80

Lys Glu Thr Asp Ser Thr Ile Val Trp Glu Asp Asp Pro Asn Arg Ser
                85                  90                  95

Tyr Thr Val Pro Ala Asn Cys Gly Gln Thr Thr Ala Ile Ile Asp Asp
            100                 105                 110
```

Thr Trp Gln
115

<210> 22
<211> 139
<212> PRT
<213> Scorias spongiosa CBM

<220>
<221> MISC_FEATURE
<222> (1)..(139)
<223> CBM

<400> 22

Ala Lys Val Pro Ser Thr Cys Ser Ala Ser Ser Ala Thr Gly Thr Cys
1 5 10 15

Thr Thr Ala Thr Ser Thr Phe Gly Gly Ser Thr Pro Thr Thr Ser Cys
20 25 30

Ala Thr Thr Pro Thr Leu Thr Thr Val Leu Phe Asn Glu Arg Ala Thr
35 40 45

Thr Asn Phe Gly Gln Asn Val His Leu Thr Gly Ser Ile Ser Gln Leu
50 55 60

Gly Ser Trp Asp Thr Asp Ser Ala Val Ala Leu Ser Ala Val Asn Tyr
65 70 75 80

Thr Ser Ser Asp Pro Leu Trp Phe Val Arg Val Gln Leu Pro Ala Gly
85 90 95

Thr Ser Phe Gln Tyr Lys Tyr Phe Lys Lys Asp Ser Ser Asn Ala Val
100 105 110

Ala Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Leu Asn Cys
115 120 125

Ala Gly Thr Ala Thr Glu Asn Asp Thr Trp Arg
130 135

<210> 23
<211> 126
<212> PRT

<213> Eupenicillium ludwigii

<220>
<221> MISC_FEATURE
<222> (1)..(126)
<223> CBM

<400> 23

```
Ser Thr Thr Thr Thr Ser Thr Thr Lys Thr Thr Thr Thr Ser Thr Thr
1               5                  10                  15

Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Ile
            20                  25                  30

Ala Thr Thr Tyr Tyr Gly Glu Asn Ile Lys Ile Ala Gly Ser Ile Ser
        35                  40                  45

Gln Leu Gly Asp Trp Asp Thr Ser Asn Ala Val Ala Leu Ser Ala Ala
    50                  55                  60

Asp Tyr Thr Ser Ser Asp His Leu Trp Phe Val Asp Ile Asp Leu Pro
65                  70                  75                  80

Ala Gly Thr Val Phe Glu Tyr Lys Tyr Ile Arg Ile Glu Ser Asp Gly
                85                  90                  95

Ser Ile Glu Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala
            100                 105                 110

Ala Cys Ala Thr Thr Ala Val Thr Glu Asn Asp Thr Trp Arg
        115                 120                 125
```

<210> 24
<211> 116
<212> PRT
<213> Aspergillus japonicus

<220>
<221> MISC_FEATURE
<222> (1)..(116)
<223> CBM

<400> 24

```
Lys Thr Ser Thr Thr Thr Ser Ser Cys Ser Thr Pro Thr Ser Val Ala
1               5                  10                  15
```

```
Val Thr Phe Asp Val Ile Ala Thr Thr Thr Tyr Gly Glu Asn Val Tyr
            20                  25                  30

Ile Ser Gly Ser Ile Ser Gln Leu Gly Ser Trp Asp Thr Ser Ser Ala
        35                  40                  45

Ile Ala Leu Ser Ala Ser Gln Tyr Thr Ser Ser Asn Asn Leu Trp Tyr
    50                  55                  60

Ala Thr Val His Leu Pro Ala Gly Thr Thr Phe Gln Tyr Lys Tyr Ile
65                  70                  75                  80

Arg Lys Glu Thr Asp Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg
                85                  90                  95

Ser Tyr Thr Val Pro Ser Ser Cys Gly Val Ser Ser Ala Thr Glu Ser
            100                 105                 110

Asp Thr Trp Arg
        115
```

<210> 25
<211> 133
<212> PRT
<213> Penicillium cf. miczynskii

<220>
<221> MISC_FEATURE
<222> (1)..(133)
<223> CBM

<400> 25

```
Thr Thr Thr Gly Gly Thr Thr Thr Ser Gln Gly Ser Thr Thr Thr Thr
1               5                   10                  15

Ser Lys Thr Ser Thr Thr Thr Ser Ser Cys Thr Ala Pro Thr Ser Val
            20                  25                  30

Ala Val Thr Phe Asp Leu Ile Ala Thr Thr Val Tyr Asp Glu Asn Val
        35                  40                  45

Gln Leu Ala Gly Ser Ile Ser Ala Leu Gly Ser Trp Asp Thr Ser Ser
    50                  55                  60
```

```
Ala Ile Arg Leu Ser Ala Ser Gln Tyr Thr Ser Ser Asn His Leu Trp
65                  70                  75                  80

Tyr Val Ala Val Ser Leu Pro Ala Gly Gln Val Phe Gln Tyr Lys Tyr
                85                  90                  95

Ile Arg Val Ala Ser Ser Gly Thr Ile Thr Trp Glu Ser Asp Pro Asn
            100                 105                 110

Leu Ser Tyr Thr Val Pro Val Ala Cys Ala Ala Thr Ala Val Thr Ile
        115                 120                 125

Ser Asp Thr Trp Arg
    130


<210>  26
<211>  116
<212>  PRT
<213>  Mz1 Penicillium sp.


<220>
<221>  MISC_FEATURE
<222>  (1)..(116)
<223>  CBM

<400>  26

Thr Lys Thr Ser Thr Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala
1               5                   10                  15

Val Thr Phe Asp Leu Ile Ala Thr Thr Thr Tyr Gly Glu Asn Ile Lys
            20                  25                  30

Ile Ala Gly Ser Ile Ala Ala Leu Gly Ala Trp Asp Thr Asp Asp Ala
        35                  40                  45

Val Ala Leu Ser Ala Ala Asp Tyr Thr Asp Ser Asp His Leu Trp Phe
    50                  55                  60

Val Thr Gln Ser Ile Pro Ala Gly Thr Val Phe Glu Tyr Lys Tyr Ile
65                  70                  75                  80

Arg Val Glu Ser Asp Gly Thr Ile Glu Trp Glu Ser Asp Pro Asn Arg
                85                  90                  95
```

```
Ser Tyr Thr Val Pro Ala Ala Cys Ala Thr Thr Ala Val Thr Glu Ser
            100                 105                 110

Asp Thr Trp Arg
        115
```

<210> 27
<211> 114
<212> PRT
<213> Thysanophora sp.

<220>
<221> MISC_FEATURE
<222> (1)..(114)
<223> CBM

<400> 27

```
Phe Thr Ser Thr Thr Lys Thr Ser Cys Thr Thr Pro Thr Ser Val Ala
1               5                   10                  15

Val Thr Phe Asp Leu Ile Ala Thr Thr Thr Tyr Gly Glu Ser Ile Arg
            20                  25                  30

Leu Val Gly Ser Ile Ser Glu Leu Gly Asp Trp Asp Thr Gly Ser Ala
        35                  40                  45

Ile Ala Leu His Ala Thr Asp Tyr Thr Asp Ser Asp His Leu Trp Phe
    50                  55                  60

Val Thr Val Gly Leu Pro Ala Gly Ala Ser Phe Glu Tyr Lys Tyr Ile
65                  70                  75                  80

Arg Val Glu Ser Ser Gly Thr Ile Glu Trp Glu Ser Asp Pro Asn Arg
                85                  90                  95

Ser Tyr Thr Val Pro Ala Ala Cys Ala Thr Thr Ala Val Thr Glu Ser
            100                 105                 110

Asp Thr
```

<210> 28
<211> 111

<212> PRT
<213> Humicola grisea var. thermoidea

<220>
<221> MISC_FEATURE
<222> (1)..(111)
<223> CBM

<400> 28

Ala Asp Ala Ser Glu Val Tyr Val Thr Phe Asn Glu Arg Val Ser Thr
1 5 10 15

Ala Trp Gly Glu Thr Ile Lys Val Val Gly Asn Val Pro Ala Leu Gly
20 25 30

Asn Trp Asp Thr Ser Lys Ala Val Thr Leu Ser Ala Ser Gly Tyr Lys
35 40 45

Ser Asn Asp Pro Leu Trp Ser Ile Thr Val Pro Ile Lys Ala Thr Gly
50 55 60

Ser Ala Val Gln Tyr Lys Tyr Ile Lys Val Gly Thr Asn Gly Lys Ile
65 70 75 80

Thr Trp Glu Ser Asp Pro Asn Arg Ser Ile Thr Leu Gln Thr Ala Ser
85 90 95

Ser Ala Gly Lys Cys Ala Ala Gln Thr Val Asn Asp Ser Trp Arg
100 105 110

<210> 29
<211> 108
<212> PRT
<213> Aspergillus niger

<220>
<221> MISC_FEATURE
<222> (1)..(108)
<223> CBM

<400> 29

Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr
1 5 10 15

Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu

20 25 30

Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr
35 40 45

Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly
50 55 60

Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val
65 70 75 80

Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys
85 90 95

Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
100 105

<210> 30
<211> 97
<212> PRT
<213> Athelia rolfsii

<220>
<221> MISC_FEATURE
<222> (1)..(97)
<223> CBM

<400> 30

Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn
1 5 10 15

Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala
20 25 30

Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr
35 40 45

Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile
50 55 60

Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile
65 70 75 80

Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu

85 90 95

Ser

<210> 31
<211> 640
<212> PRT
<213> Aspergillus kawachi alpha-amylase

<220>
<221> mat_peptide
<222> (22)..(640)

<400> 31

Met Arg Val Ser Thr Ser Ser Ile Ala Leu Ala Val Ser Leu Phe Gly
-20 -15 -10

Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile
-5 -1 1 5 10

Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
15 20 25

Ala Thr Cys Asn Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln
30 35 40

Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
45 50 55

Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ser Asp
60 65 70 75

Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Tyr Val Asn
80 85 90

Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu
95 100 105

His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
110 115 120

Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
125 130 135

```
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
140                 145                 150                 155

Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val
                160                 165                 170

Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp
            175                 180                 185

Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
        190                 195                 200

Arg Ile Asp Ser Val Glu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
    205                 210                 215

Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
220                 225                 230                 235

Pro Ala Leu Asp Cys Pro Tyr Gln Lys Tyr Leu Asp Gly Val Leu Asn
                240                 245                 250

Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
            255                 260                 265

Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
        270                 275                 280

Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
    285                 290                 295

Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
300                 305                 310                 315

Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
                320                 325                 330

Glu Gln His Tyr Ser Gly Gly Asp Val Pro Tyr Asn Arg Glu Ala Thr
            335                 340                 345

Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala
        350                 355                 360
```

```
Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Asp Tyr
    365                 370                 375

Ile Thr Tyr Lys Asn Asp Pro Ile Tyr Thr Asp Ser Asn Thr Ile Ala
380                 385                 390                 395

Met Arg Lys Gly Thr Ser Gly Ser Gln Ile Ile Thr Val Leu Ser Asn
                400                 405                 410

Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly
            415                 420                 425

Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val
        430                 435                 440

Thr Val Asp Ser Asn Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu
    445                 450                 455

Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys
460                 465                 470                 475

Gly Gly Ser Gly Asn Thr Thr Thr Thr Thr Thr Ala Ala Thr Ser Thr
                480                 485                 490

Ser Lys Ala Thr Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr
            495                 500                 505

Ser Ser Ser Cys Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu
        510                 515                 520

Glu Leu Val Thr Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser
    525                 530                 535

Ile Ser Gln Leu Gly Glu Trp His Thr Ser Asp Ala Val Lys Leu Ser
540                 545                 550                 555

Ala Asp Asp Tyr Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser
                560                 565                 570

Leu Pro Val Gly Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu
            575                 580                 585
```

```
Gly Gly Ser Val Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val
        590                 595                 600

Pro Glu Cys Gly Ser Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
    605                 610                 615
```

<210> 32
<211> 1860
<212> DNA
<213> Artificial

<220>
<223> hybrid consisting of Aspergillus niger acid alpha-amylase catalytic domain-Aspergillus kawachii alpha-amylase linker-Aspergillus niger glucoamylase CBM

<220>
<221> CDS
<222> (1)..(1860)
<223> hybrid

<400> 32

```
ctg tcg gct gca gaa tgg cgc act cag tcg att tac ttc cta ttg acg       48
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15

gat cgg ttc ggt agg acg gac aat tcg acg aca gct aca tgc gat acg       96
Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30

ggt gac caa atc tat tgt ggt ggc agt tgg caa gga atc atc aac cat      144
Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45

ctg gat tat atc cag ggc atg gga ttc acg gcc atc tgg atc tcg cct      192
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60

atc act gaa cag ctg ccc cag gat act gct gat ggt gaa gct tac cat      240
Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80

gga tat tgg cag cag aag ata tac gac gtg aac tcc aac ttc ggc act      288
Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95

gca gat gac ctc aag tcc ctc tca gat gcg ctt cat gcc cgc gga atg      336
Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110

tac ctc atg gtg gac gtc gtc cct aac cac atg ggc tac gcc ggc aac      384
Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125
```

```
ggc aac gat gta gac tac agc gtc ttc gac ccc ttc gat tcc tcc tcc      432
Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140

tac ttc cac cca tac tgc ctg atc aca gat tgg gac aac ttg acc atg      480
Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160

gtc caa gat tgt tgg gag ggt gac acc atc gta tct ctg cca gac cta      528
Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175

aac acc acc gaa act gcc gtg aga aca atc tgg tat gac tgg gta gcc      576
Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190

gac ctg gta tcc aat tat tca gtc gac gga ctc cgc atc gac agt gtc      624
Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205

ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac cag gaa gca gca ggt      672
Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220

gtc tac tgc gtc ggc gaa gtc gac aac ggc aac cct gcc ctc gac tgc      720
Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240

cca tac cag aag gtc ctg gac ggc gtc ctc aac tat ccg atc tac tgg      768
Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255

caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc agc atc agc aat ctc      816
Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270

tac aac atg atc aaa tcc gtc gca agc gac tgc tcc gat ccg aca cta      864
Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285

ctc ggc aac ttc atc gaa aac cac gac aat ccc cgt ttc gcc tcc tac      912
Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

acc tcc gac tac tcg caa gcc aaa aac gtc ctc agc tac atc ttc ctc      960
Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320

tcc gac ggc atc ccc atc gtc tac gcc ggc gaa gaa cag cac tac tcc     1008
Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335

ggc ggc aag gtg ccc tac aac cgc gaa gcg acc tgg ctt tca ggc tac     1056
Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

gac acc tcc gca gag ctg tac acc tgg ata gcc acc acg aac gcg atc     1104
```

```
Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365

cgc aaa cta gcc atc tca gct gac tcg gcc tac att acc tac gcg aat     1152
Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
    370                 375                 380

gat gca ttc tac act gac agc aac acc atc gca atg cgc aaa ggc acc     1200
Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

tca ggg agc caa gtc atc acc gtc ctc tcc aac aaa ggc tcc tca gga     1248
Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
                405                 410                 415

agc agc tac acc ctg acc ctc agc gga agc ggc tac aca tcc ggc acg     1296
Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
            420                 425                 430

aag ctg atc gaa gcg tac aca tgc aca tcc gtg acc gtg gac tcg agc     1344
Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445

ggc gat att ccc gtg ccg atg gcg tcg gga tta ccg aga gtt ctt ctg     1392
Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
    450                 455                 460

ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt ggc ggg agc gga aga     1440
Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465                 470                 475                 480

aca acc acg acc aca act gct gct gct act agt aca tcc aaa gcc acc     1488
Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
                485                 490                 495

acc tcc tct tct tct tct tct gct gct gct act act tct tca tca tgt     1536
Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys
            500                 505                 510

acc act ccc acc gcc gtg gct gtg act ttc gat ctg aca gct acc acc     1584
Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr Thr
        515                 520                 525

acc tac ggc gag aac atc tac ctg gtc gga tcg atc tct cag ctg ggt     1632
Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly
    530                 535                 540

gac tgg gaa acc agc gac ggc ata gct ctg agt gct gac aag tac act     1680
Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr
545                 550                 555                 560

tcc agc gac ccg ctc tgg tat gtc act gtg act ctg ccg gct ggt gag     1728
Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu
                565                 570                 575

tcg ttt gag tac aag ttt atc cgc att gag agc gat gac tcc gtg gag     1776
Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu
```

```
          580                 585                 590

tgg gag agt gat ccc aac cga gaa tac acc gtt cct cag gcg tgc gga     1824
Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly
        595                 600                 605

acg tcg acc gcg acg gtg act gac acc tgg cgg tag                     1860
Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
    610                 615
```

<210> 33
<211> 619
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 33

```
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15

Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30

Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95

Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110

Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140
```

```
Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160

Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175

Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205

Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220

Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365

Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
```

370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465 470 475 480

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
485 490 495

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys
500 505 510

Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala Thr Thr
515 520 525

Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly
530 535 540

Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr
545 550 555 560

Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu
565 570 575

Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu
580 585 590

Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly
595 600 605

```
Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
    610                 615


<210>  34
<211>  1827
<212>  DNA
<213>  Artificial

<220>
<223>  Hybrid containing Aspergillus niger acid alpha-amylase catalytic
       domain-Aspergillus kawachii alpha-amylase linker-Athelia rolfsii
       glucoamylase CBD


<220>
<221>  CDS
<222>  (1)..(1827)
<223>  Hybrid

<400>  34
ctg tcg gct gca gaa tgg cgc act cag tcg att tac ttc cta ttg acg       48
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15

gat cgg ttc ggt agg acg gac aat tcg acg aca gct aca tgc gat acg       96
Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30

ggt gac caa atc tat tgt ggt ggc agt tgg caa gga atc atc aac cat      144
Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45

ctg gat tat atc cag ggc atg gga ttc acg gcc atc tgg atc tcg cct      192
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60

atc act gaa cag ctg ccc cag gat act gct gat ggt gaa gct tac cat      240
Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80

gga tat tgg cag cag aag ata tac gac gtg aac tcc aac ttc ggc act      288
Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95

gca gat gac ctc aag tcc ctc tca gat gcg ctt cat gcc cgc gga atg      336
Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110

tac ctc atg gtg gac gtc gtc cct aac cac atg ggc tac gcc ggc aac      384
Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125

ggc aac gat gta gac tac agc gtc ttc gac ccc ttc gat tcc tcc tcc      432
Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
```

```
    130                 135                 140

tac ttc cac cca tac tgc ctg atc aca gat tgg gac aac ttg acc atg      480
Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160

gtc caa gat tgt tgg gag ggt gac acc atc gta tct ctg cca gac cta      528
Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175

aac acc acc gaa act gcc gtg aga aca atc tgg tat gac tgg gta gcc      576
Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190

gac ctg gta tcc aat tat tca gtc gac gga ctc cgc atc gac agt gtc      624
Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205

ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac cag gaa gca gca ggt      672
Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220

gtc tac tgc gtc ggc gaa gtc gac aac ggc aac cct gcc ctc gac tgc      720
Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240

cca tac cag aag gtc ctg gac ggc gtc ctc aac tat ccg atc tac tgg      768
Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255

caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc agc atc agc aat ctc      816
Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270

tac aac atg atc aaa tcc gtc gca agc gac tgc tcc gat ccg aca cta      864
Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285

ctc ggc aac ttc atc gaa aac cac gac aat ccc cgt ttc gcc tcc tac      912
Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

acc tcc gac tac tcg caa gcc aaa aac gtc ctc agc tac atc ttc ctc      960
Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320

tcc gac ggc atc ccc atc gtc tac gcc ggc gaa gaa cag cac tac tcc     1008
Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335

ggc ggc aag gtg ccc tac aac cgc gaa gcg acc tgg ctt tca ggc tac     1056
Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

gac acc tcc gca gag ctg tac acc tgg ata gcc acc acg aac gcg atc     1104
Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365
```

```
cgc aaa cta gcc atc tca gct gac tcg gcc tac att acc tac gcg aat     1152
Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
    370                 375                 380

gat gca ttc tac act gac agc aac acc atc gca atg cgc aaa ggc acc     1200
Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

tca ggg agc caa gtc atc acc gtc ctc tcc aac aaa ggc tcc tca gga     1248
Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
                405                 410                 415

agc agc tac acc ctg acc ctc agc gga agc ggc tac aca tcc ggc acg     1296
Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
            420                 425                 430

aag ctg atc gaa gcg tac aca tgc aca tcc gtg acc gtg gac tcg agc     1344
Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445

ggc gat att ccc gtg ccg atg gcg tcg gga tta ccg aga gtt ctt ctg     1392
Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
    450                 455                 460

ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt ggc ggg agc gga aga     1440
Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465                 470                 475                 480

aca acc acg acc aca act gct gct gct act agt aca tcc aaa gcc acc     1488
Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
                485                 490                 495

acc tcc tct tct tct tct tct gct gct gct act act tct tca tca gtc     1536
Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Val
            500                 505                 510

gag gtc act ttc gac gtt tac gct acc aca gta tat ggc cag aac atc     1584
Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile
        515                 520                 525

tat atc acc ggt gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat     1632
Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn
    530                 535                 540

ggt gtt gca ctc tct tct gct aac tac ccc acc tgg agt gcc acg atc     1680
Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile
545                 550                 555                 560

gct ctc ccc gct gac acg aca atc cag tac aag tat gtc aac att gac     1728
Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp
                565                 570                 575

ggc agc acc gtc atc tgg gag gat gct atc agc aat cgc gag atc acg     1776
Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr
            580                 585                 590
```

```
acg ccc gcc agc ggc aca tac acc gaa aaa gac act tgg gat gaa tct      1824
Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
        595                 600                 605

tag                                                                  1827
```

<210> 35
<211> 608
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 35

```
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                  10                  15

Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30

Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95

Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110

Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160
```

```
Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175

Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205

Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220

Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365

Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
    370                 375                 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
```

385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
450 455 460

Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465 470 475 480

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
485 490 495

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Val
500 505 510

Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile
515 520 525

Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn
530 535 540

Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile
545 550 555 560

Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp
565 570 575

Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr
580 585 590

Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
595 600 605

<210> 36
<211> 1863

<212> DNA
<213> Artificial

<220>
<223> Hybrid consisting of A.oryzae alpha-amylase catalytic domain-A. kawachii alpha-amylase linker-A. kawachi alpha-amylase CBD

<220>
<221> CDS
<222> (1)..(1863)
<223> Hybrid

<400> 36

```
gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc ctt ctc acg       48
Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15

gat cga ttt gca agg acg gat ggg tcg acg act gcg act tgt aat act       96
Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30

gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc atc gac aag      144
Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45

ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg atc acc ccc      192
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60

gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat gcc tac cat      240
Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65                  70                  75                  80

ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac tac ggc act      288
Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95

gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat gag agg ggg atg      336
Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110

tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat gat gga gcg      384
Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125

ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt tcc caa gac      432
Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
    130                 135                 140

tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat cag act cag      480
Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145                 150                 155                 160

gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg cct gat ctc      528
Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165                 170                 175
```

```
gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac tgg gtg gga      576
Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180                 185                 190

tca ttg gta tcg aac tac tcc att gac ggc ctc cgt atc gac aca gta      624
Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205

aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa gcc gca ggc      672
Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220

gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc tac act tgt      720
Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240

ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc att tac tat      768
Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255

cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg gac gac ctc      816
Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270

tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac tca aca ctc      864
Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc gct tct tac      912
Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc atc atc ctc      960
Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320

aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag cac tac gcc     1008
Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335

ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc tcg ggc tac     1056
Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg aac gca atc     1104
Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
        355                 360                 365

cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc tac aag aac     1152
Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380

tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc aag ggc aca     1200
Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400
```

```
gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt gct tcg ggt     1248
Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415

gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca gcc ggc cag     1296
Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
            420                 425                 430

caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt ggt tcg gat     1344
Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445

gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg gta ttg tat     1392
Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460

ccg act gag aag ttg gca ggt agc aag atc tgt agt agc tcg gga aga     1440
Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
465                 470                 475                 480

aca acc acg acc aca act gct gct gct act agt aca tcc aaa gcc acc     1488
Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
                485                 490                 495

acc tcc tct tct tct tct tct gct gct gct act act tct tca tca tgc     1536
Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys
            500                 505                 510

acc gca aca agc acc acc ctc ccc atc acc ttc gaa gaa ctc gtc acc     1584
Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu Glu Leu Val Thr
        515                 520                 525

act acc tac ggg gaa gaa gtc tac ctc agc gga tct atc tcc cag ctc     1632
Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser Ile Ser Gln Leu
    530                 535                 540

gga gag tgg gat acg agt gac gcg gtg aag ttg tcc gcg gat gat tat     1680
Gly Glu Trp Asp Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp Tyr
545                 550                 555                 560

acc tcg agt aac ccc gag tgg tct gtt act gtg tcg ttg ccg gtg ggg     1728
Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser Leu Pro Val Gly
                565                 570                 575

acg acc ttc gag tat aag ttt att aag gtc gat gag ggt gga agt gtg     1776
Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu Gly Gly Ser Val
            580                 585                 590

act tgg gaa agt gat ccg aat agg gag tat act gtg cct gaa tgt ggg     1824
Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys Gly
        595                 600                 605

aat ggg agt ggg gag acg gtg gtt gat acg tgg agg tag                 1863
Asn Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
    610                 615                 620
```

<210> 37
<211> 620
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 37

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1 5 10 15

Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
20 25 30

Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
50 55 60

Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65 70 75 80

Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
85 90 95

Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
100 105 110

Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
115 120 125

Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
130 135 140

Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145 150 155 160

Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
165 170 175

Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
180 185 190

```
Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205

Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220

Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240

Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255

Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270

Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320

Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335

Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
        355                 360                 365

Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380

Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415
```

```
Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
            420                 425                 430

Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445

Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460

Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
465                 470                 475                 480

Thr Thr Thr Thr Thr Thr Ala Ala Ala Thr Ser Thr Ser Lys Ala Thr
                485                 490                 495

Thr Ser Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys
            500                 505                 510

Thr Ala Thr Ser Thr Thr Leu Pro Ile Thr Phe Glu Glu Leu Val Thr
        515                 520                 525

Thr Thr Tyr Gly Glu Glu Val Tyr Leu Ser Gly Ser Ile Ser Gln Leu
    530                 535                 540

Gly Glu Trp Asp Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp Tyr
545                 550                 555                 560

Thr Ser Ser Asn Pro Glu Trp Ser Val Thr Val Ser Leu Pro Val Gly
                565                 570                 575

Thr Thr Phe Glu Tyr Lys Phe Ile Lys Val Asp Glu Gly Gly Ser Val
            580                 585                 590

Thr Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys Gly
        595                 600                 605

Asn Gly Ser Gly Glu Thr Val Val Asp Thr Trp Arg
    610                 615                 620
```

<210> 38
<211> 1767
<212> DNA
<213> Artificial

<220>
<223> Hybrid consisting of A. niger acid alpha-amylase catalytic domain- A.rolfsii glucoamylase linker- A. rolfsii glucoamylase CBM

<220>
<221> CDS
<222> (1)..(1767)
<223> Hybrid

<400> 38

```
ctg tcg gct gca gaa tgg cgc act cag tcg att tac ttc cta ttg acg       48
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15

gat cgg ttc ggt agg acg gac aat tcg acg aca gct aca tgc gat acg       96
Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30

ggt gac caa atc tat tgt ggt ggc agt tgg caa gga atc atc aac cat      144
Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45

ctg gat tat atc cag ggc atg gga ttc acg gcc atc tgg atc tcg cct      192
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60

atc act gaa cag ctg ccc cag gat act gct gat ggt gaa gct tac cat      240
Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80

gga tat tgg cag cag aag ata tac gac gtg aac tcc aac ttc ggc act      288
Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95

gca gat gac ctc aag tcc ctc tca gat gcg ctt cat gcc cgc gga atg      336
Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110

tac ctc atg gtg gac gtc gtc cct aac cac atg ggc tac gcc ggc aac      384
Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125

ggc aac gat gta gac tac agc gtc ttc gac ccc ttc gat tcc tcc tcc      432
Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140

tac ttc cac cca tac tgc ctg atc aca gat tgg gac aac ttg acc atg      480
Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160

gtc caa gat tgt tgg gag ggt gac acc atc gta tct ctg cca gac cta      528
Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175

aac acc acc gaa act gcc gtg aga aca atc tgg tat gac tgg gta gcc      576
```

```
Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190

gac ctg gta tcc aat tat tca gtc gac gga ctc cgc atc gac agt gtc      624
Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205

ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac cag gaa gca gca ggt      672
Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220

gtc tac tgc gtc ggc gaa gtc gac aac ggc aac cct gcc ctc gac tgc      720
Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240

cca tac cag aag gtc ctg gac ggc gtc ctc aac tat ccg atc tac tgg      768
Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255

caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc agc atc agc aat ctc      816
Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270

tac aac atg atc aaa tcc gtc gca agc gac tgc tcc gat ccg aca cta      864
Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285

ctc ggc aac ttc atc gaa aac cac gac aat ccc cgt ttc gcc tcc tac      912
Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

acc tcc gac tac tcg caa gcc aaa aac gtc ctc agc tac atc ttc ctc      960
Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320

tcc gac ggc atc ccc atc gtc tac gcc ggc gaa gaa cag cac tac tcc     1008
Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335

ggc ggc aag gtg ccc tac aac cgc gaa gcg acc tgg ctt tca ggc tac     1056
Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

gac acc tcc gca gag ctg tac acc tgg ata gcc acc acg aac gcg atc     1104
Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365

cgc aaa cta gcc atc tca gct gac tcg gcc tac att acc tac gcg aat     1152
Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
    370                 375                 380

gat gca ttc tac act gac agc aac acc atc gca atg cgc aaa ggc acc     1200
Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

tca ggg agc caa gtc atc acc gtc ctc tcc aac aaa ggc tcc tca gga     1248
Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
```

```
                405                 410                 415

agc agc tac acc ctg acc ctc agc gga agc ggc tac aca tcc ggc acg     1296
Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
            420                 425                 430

aag ctg atc gaa gcg tac aca tgc aca tcc gtg acc gtg gac tcg agc     1344
Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445

ggc gat att ccc gtg ccg atg gcg tcg gga tta ccg aga gtt ctt ctg     1392
Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
    450                 455                 460

ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt ggc ggg agc gga aga     1440
Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465                 470                 475                 480

ggt gct aca agc ccg ggt ggc tcc tcg ggt agt gtc gag gtc act ttc     1488
Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495

gac gtt tac gct acc aca gta tat ggc cag aac atc tat atc acc ggt     1536
Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510

gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat ggt gtt gca ctc     1584
Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525

tct tct gct aac tac ccc acc tgg agt gcc acg atc gct ctc ccc gct     1632
Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
    530                 535                 540

gac acg aca atc cag tac aag tat gtc aac att gac ggc agc acc gtc     1680
Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560

atc tgg gag gat gct atc agc aat cgc gag atc acg acg ccc gcc agc     1728
Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575

ggc aca tac acc gaa aaa gac act tgg gat gaa tct tag                 1767
Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585
```

<210> 39
<211> 588
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 39

```
Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                  10                  15

Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30

Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60

Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80

Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95

Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110

Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125

Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140

Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160

Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175

Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190

Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205

Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220

Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
```

225 230 235 240

Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
245 250 255

Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
260 265 270

Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
275 280 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
290 295 300

Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305 310 315 320

Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
325 330 335

Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
340 345 350

Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
355 360 365

Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
370 375 380

Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385 390 395 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
405 410 415

Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
420 425 430

Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
435 440 445

Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
450 455 460

```
Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465                 470                 475                 480

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495

Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510

Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
    530                 535                 540

Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560

Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575

Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585
```

<210> 40
<211> 1767
<212> DNA
<213> Artificial

<220>
<223> Hybrid containing A. oryzae alpha-amylase catalytic domain- A. rolfsii glucoamylase linker- A. rolfsii glucoamylase CBM

<220>
<221> CDS
<222> (1)..(1767)
<223> Hybrid

<400> 40

```
gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc ctt ctc acg       48
Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15

gat cga ttt gca agg acg gat ggg tcg acg act gcg act tgt aat act       96
Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30
```

```
gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc atc gac aag      144
Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45

ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg atc acc ccc      192
Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60

gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat gcc tac cat      240
Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65                  70                  75                  80

ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac tac ggc act      288
Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95

gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat gag agg ggg atg      336
Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110

tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat gat gga gcg      384
Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125

ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt tcc caa gac      432
Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
    130                 135                 140

tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat cag act cag      480
Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145                 150                 155                 160

gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg cct gat ctc      528
Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165                 170                 175

gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac tgg gtg gga      576
Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180                 185                 190

tca ttg gta tcg aac tac tcc att gac ggc ctc cgt atc gac aca gta      624
Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205

aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa gcc gca ggc      672
Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220

gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc tac act tgt      720
Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240

ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc att tac tat      768
Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255
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cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg gac gac ctc      816
Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270

tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac tca aca ctc      864
Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc gct tct tac      912
Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc atc atc ctc      960
Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320

aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag cac tac gcc     1008
Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335

ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc tcg ggc tac     1056
Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg aac gca atc     1104
Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
        355                 360                 365

cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc tac aag aac     1152
Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380

tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc aag ggc aca     1200
Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt gct tcg ggt     1248
Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415

gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca gcc ggc cag     1296
Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
            420                 425                 430

caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt ggt tcg gat     1344
Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445

gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg gta ttg tat     1392
Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460

ccg act gag aag ttg gca ggt agc aag atc tgt agt agc tcg gga aga     1440
Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
465                 470                 475                 480

ggt gct aca agc ccg ggt ggc tcc tcg ggt agt gtc gag gtc act ttc     1488
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Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495

gac gtt tac gct acc aca gta tat ggc cag aac atc tat atc acc ggt     1536
Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510

gat gtg agt gag ctc ggc aac tgg aca ccc gcc aat ggt gtt gca ctc     1584
Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525

tct tct gct aac tac ccc acc tgg agt gcc acg atc gct ctc ccc gct     1632
Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
    530                 535                 540

gac acg aca atc cag tac aag tat gtc aac att gac ggc agc acc gtc     1680
Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560

atc tgg gag gat gct atc agc aat cgc gag atc acg acg ccc gcc agc     1728
Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575

ggc aca tac acc gaa aaa gac act tgg gat gaa tct tag                 1767
Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585
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<213> Artificial

<220>
<223> Synthetic Construct

<400> 41

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Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15

Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30

Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60

Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65                  70                  75                  80
```

```
Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95

Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110

Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125

Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
    130                 135                 140

Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145                 150                 155                 160

Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165                 170                 175

Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180                 185                 190

Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205

Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220

Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240

Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255

Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270

Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300
```

```
Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320

Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335

Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
        355                 360                 365

Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380

Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415

Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
            420                 425                 430

Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445

Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460

Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
465                 470                 475                 480

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495

Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510

Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
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530 535 540

Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545 550 555 560

Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
565 570 575

Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
580 585